

46

(vii) IMMEDIATE SOURCE:

RAW SEQUENCE LISTING PATENT APPLICATION US/08/915,659A

DATE: 05/01/98 TIME: 12:50:57

INPUT SET: S25500.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

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SEQUENCE LISTING
    (1)
           General Information:
     (i)APPLICANT: O'Brien et al
 4
     (ii) TITLE OF INVENTION: Novel Extracellular Serine Protease
 5
    (iii) NUMBER OF SEQUENCES: 10
 6
    (iv) CORRESPONDENCE ADDRESS:
 7
 8
    (A) ADDRESSEE: Benjamin Aaron Adler, Ph.D. J.D.
 9
    (B)STREET: 8011 Candle Lane
10
    (C)CITY: Houston
11
    (D)STATE: Texas
12
    (E) COUNTRY: USA
13
    (F)ZIP: 77071
14
    (v) COMPUTER READABLE FORM:
15
     (A) MEDIUM TYPE: 1.44 Mb floppy disk
    (B) COMPUTER: Apple Macintosh
16
17
    (C) OPERATING SYSTEM: Macintosh
18
    (D)SOFTWARE: Microsoft Word for Macintosh
    (vi)CURRENT APPLICATION DATA:
19
    (A)APPLICATION NUMBER: 08/915,659
20
21
    (B) FILING DATE: August 21, 1997
22
    (C)CLASSIFICATION: 435
23
    (vii)PRIOR APPLICATION DATE:
24
    (A) APPLICATION NUMBER:
25
    (B) FILING DATE:
26
    (viii) ATTORNEY/AGENT INFORMATION:
27
    (A) NAME: Benjamin Aaron Adler, Ph.D.
28
    (B) REGISTRATION NUMBER: 35,423
29
    (C)REFERENCE/DOCKET NUMBER: D6020
30
    (ix) TELECOMMUNICATION INFORMATION:
31
    (A) TELEPHONE: (713) 777-2321
32
    (B) TELEFAX: (713) 777-6908
33
34
    (2) INFORMATION FOR SEQ ID NO:1:
35
    (i) SEQUENCE CHARACTERISTICS:
36
    (A) LENGTH: 144 amino acids
37
    (B) TYPE: amino acid
38
    (C) STRANDEDNESS:
39
    (D) TOPOLOGY: linear
40
    (ii) MOLECULE TYPE:
    (A) DESCRIPTION: protein
41
42
    (iii) HYPOTHETICAL: no
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    (iv) ANTI-SENSE: no
    (v) FRAGMENT TYPE: internal
44
45
    (vi) ORIGINAL SOURCE:
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/915,659A

DATE: 05/01/98 TIME: 12:50:58

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(viii) POSITION IN GENOME:
47
    (ix) FEATURE:
48
49
    (x) PUBLICATION INFORMATION:
50
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    Trp Val Leu Thr Ala Ala His Cys Lys Pro Asn Leu Gln Val
51
52
53
54
    Phe Leu Glu Lys His Asn Leu Arg Gln Arg Glu Ser Ser Gln Glu
55
                                         25
56
    Gln Ser Ser Val Val Arg Ala Val Ile His Pro Asp Tyr Asp Ala
57
58
59
60
    Ala Ser His Asp Gln Asp Ile Met Leu Leu Arg Leu Ala Arg Pro
61
62
    Ala Lys Leu Ser Glu Leu Ile Gln Pro Leu Pro Leu Glu Arg Asp
63
64
65
66
    Cys Ser Ala Asn Thr Thr Ser Cys His Ile Leu Gly Trp Gly Lys
67
                                         85
68
69
70
    Thr Ala Asp Gly Asp Phe Pro Asp Thr Ile Gln Cys Ala Tyr Ile
71
                     95
                                         100
72
    His Leu Val Ser Arg Glu Glu Cys Glu His Ala Tyr Pro Gly Gln
73
74
75
76
    Ile Thr Gln Asn Met Leu Cys Ala Gln Asp Glu Lys Tyr Gly Lys
77
                                         130
78
79
    Asp Ser Cys Gln Gly Asp Ser Gly Gly
80
    (2) INFORMATION FOR SEQ ID NO:2:
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    (i) SEQUENCE CHARACTERISTICS:
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    (A) LENGTH: 148 amino acids
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    (B) TYPE: amino acid
84
    (C) STRANDEDNESS:
85
    (D) TOPOLOGY: linear
86
87
    (ii) MOLECULE TYPE:
    (A) DESCRIPTION: protein
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    (iii) HYPOTHETICAL: no
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    (iv) ANTI-SENSE: no
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    (v) FRAGMENT TYPE: internal
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    (vi) ORIGINAL SOURCE:
93
    (vii) IMMEDIATE SOURCE:
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    (viii) POSITION IN GENOME:
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    (ix) FEATURE:
    (x) PUBLICATION INFORMATION:
96
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    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:
98
    Trp Val Val Thr Ala Ala His Cys Lys Pro Lys Tyr Thr Val
99
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RAW SEQUENCE LISTING PATENT APPLICATION US/08/915,659A

DATE: 05/01/98 TIME: 12:50:59

100															
101	Arg	Leu	Gly	Asp	His	Ser	Leu	Gln	Asn	Lys	Asp	Gly	Pro	Glu	Gln
102					20					25					30
103															
104	Glu	Ile	Pro	Val	Val	Gln	Ser	Ile	Pro	His	Pro	Cys	Tyr	Asn	Ser
105					35					40					45
106															
107	Ser	Asp	Val	Glu	Asp	His	Asn	His	Asp	Leu	Met	Leu	Leu	Gln	Leu
108					50					55					60
109															
110	Arg	Asp	Gln	Ala	Ser	Leu	Gly	Ser	Lys	Val	Lys	Pro	Ile	Ser	Leu
111					65					70					75
112															
113	Ala	Asp	His	Cys	Thr	Gln	Pro	Gly	Gln	Asn	Cys	Thr	Val	Ser	Gly
114					80					85					90
115															
116	Trp	Gly	Thr	Val	Thr	Ser	Pro	Arg	Glu	Asn	Phe	Pro	Asp	Thr	Leu
117					95					100					105
118															
119	Asn	Cys	Ala	Glu	Val	Lys	Ile	Phe	Pro	Gln	Lys	Lys	Cys	Glu	Asp
120					110					115					120
121															
122	Ala	Tyr	Pro	Gly	Gln	Ile	Thr	Asp	Gly	Met	Val	Cys	Ala	Gly	Ser
123					125					130					135
124															
125	Ser	Lys	Gly	Ala	Asp	Thr	Cys	Gln	Gly	Asp	Ser	Gly	Gly		
126					140					145					
127							ID N		:						
128	(i)	SEQU	JENCE	CHA	ARACI	TERIS	STICS	:							
129	(A)	LENG	GTH:	146	am i	ino a	acids	5							
130	(B)	TYPE	3: a	amino	aci	lđ									
131			ANDEI		3:										
132			DLOGY		linea	ar									
133	(ii)	MOI	LECUI	E T	PE:										
134	• •				pr		.n								
135	-	-			CAL:	no									
136			ri-se												
137			3MEN1				ernal	-							
138					URCE										
139					SOUF										
140	•	•			IN C	ENON	1E :								
141	(ix)														
142							NOI:								
143							N:SE						_	_	_
144	Trp	Val	Val	Ser		Gly	His	Cys	Tyr		Ser	Arg	Ile	Gln	
145					5					10					15
146															
147			_				_								
148	Arg	Leu	Gly	Glu		Asn	Ile	Glu	Val		Glu	Gly	Asn	Glu	
149					20					25					30
150															
			_			_	_ ~		_					_	
151 152	Phe	Ile	Asn	Ala		Lys	Ile	Ile	Arg		Pro	Gln	Tyr	Asp	

RAW SEQUENCE LISTING PATENT APPLICATION US/08/915,659A

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														I I	NPUT SE
153 154 155 156	Lys	Thr	Leu	Asn	Asn 50	Asp	Ile	Met	Leu	Ile 55	Lys	Leu	Ser	Ser	Arg 60
157 158 159	Ala	Val	Ile	Asn	Ala 65	Arg	Val	Ser	Thr	Ile 70	Ser	Leu	Pro	Thr	Ala 75
160 161 162	Pro	Pro	Ala	Thr	Gly 80	Thr	Lys	Cys	Leu	Ile 85	Ser	Gly	Trp	Gly	Asn 90
163 164 165	Thr	Ala	Ser	Ser	Gly 95	Ala	Asp	Tyr	Pro	Asp 100	Glu	Leu	Gln	Cys	Leu 105
166 167 168	Asp	Ala	Pro	Val	Leu 110	Ser	Gln	Ala	Lys	Cys 115	Glu	Ala	Ser	Tyr	Pro 120
169 170 171	Gly	Lys	Ile	Thr	Ser 125	Asn	Met	Phe	Cys	Val 130	Gly	Phe	Leu	Glu	Gly 135
172 173 174	Gly	Lys	Asp	Ser	Cys 140	Gln	Gly	Asp	Ser	Gly 145	Gly				
175 176 177 178 179 180 181 182 183 184 185 186 187 188	(i) (A) (B) (C) (D) (ii (iv (v) (vi (vi (vi (ix	SEQUENCE TYPE STRATE TOPE DESCRIPTION AND TRACE OF THE SECRIPT STRATE TO THE SECRIPT STR		E CHA 144 amino DNESS LE TY FION: ENSE: F TYP AL SO LATE FION EST LE TYP LE	ARACTIA amino acionica con acio	rerisino a ino a cotei no inte	STICS acids in ernal		•						
191	. ,		QUENC						NO:	: 4	l :				
192 193 194	Trp	Val	Leu	Thr	Ala 5	Ala	His	Суs	Lys	Met 10	Asn	Glu	Tyr	Thr	Val 15
195 196 197	His	Leu	Gly	Ser	Asp 20	Thr	Leu	Gly	Asp	Arg 25	Arg	Ala	Gln	Arg	Ile 30
198 199 200	Lys	Ala	Ser	Lys	Ser 35	Phe	Arg	His	Pro	Gly 40	Tyr	Ser	Thr	Gln	Thr 45
201 202 203			Asn		50					55					60
204 205	Leu	Ser	Ser	Met	Val 65	Lys	Lys	Val	Arg	Leu 70	Pro	Ser	Arg	Cys	Glu 75

RAW SEQUENCE LISTING PATENT APPLICATION US/08/915,659A

DATE: 05/01/98 TIME: 12:51:00

209 210 Ser Pro Asp Val Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val 211 95 100 100 212 213 Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Let 110 115 125 216 Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Ly 125 130 130 217 128 Asn Ala Cys Asn Gly Asp Ser Gly Gly 120 140 221 (2) INFORMATION FOR SEQ ID NO:5: 223 (i) SEQUENCE CHARACTERISTICS: 224 (A) LENGTH: 159 amino acids 225 (B) TYPE: amino acid 226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSTION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Ser 243 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 250 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty															I I	VPUI 3
209 210 Ser Pro Asp Val Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val 211 212 213 Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Le 110 214 110 215 216 Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Ly 125 217 128 218 Asn Ala Cys Asn Gly Asp Ser Gly Gly 130 219 Asn Ala Cys Asn Gly Asp Ser Gly Gly 140 221 222 (2) INFORMATION FOR SEQ ID NO:5: 223 (i) SEQUENCE CHARACTERISTICS: 224 (A) LENGTH: 159 amino acids 225 (B) TYPE: amino acid 226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSTION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Ser 243 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 25 247 Cly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 250 50 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 253 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	-	Pro	Pro	Gly	Thr	Thr	Cys	Thr	Val	Ser	Gly	Trp	Gly	Thr	Thr	Thr
210 Ser Pro Asp Val Thr Phe Pro Ser Asp Leu Met Cys Val Asp Val 211 20						80					85					90
Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Let	210	Ser	Pro	Asp	Val		Phe	Pro	Ser	Asp		Met	Cys	Val	Asp	
Lys Leu Ile Ser Pro Gln Asp Cys Thr Lys Val Tyr Lys Asp Le						95					100					105
214		T	T	T1_	~~	D=0	al =	1 am	a	mb ~	T	W-1	M	T ***	3 am	T 011
Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Ly		гàг	Leu	тте	ser		GIN	Asp	Cys	Thr	_	vaı	туг	гуѕ	ASP	
Leu Glu Asn Ser Met Leu Cys Ala Gly Ile Pro Asp Ser Lys Ly						110					113					120
217 218 219 219 219 220 210 221 220 221 222 (2) INFORMATION FOR SEQ ID NO:5: 223 (i) SEQUENCE CHARACTERISTICS: 224 (A) LENGTH: 159 amino acids 225 (B) TYPE: amino acid 226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 238 (ii) MOLECULE TYPE: 249 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 240 25 241 242 245 240 25 26 27 284 285 297 298 299 299 290 299 290 290 290 290 290 291 291 292 293 293 294 295 297 298 299 299 290 290 290 290 290 290 291 291 292 290 290 290 290 291 291 292 293 293 294 295 297 298 299 299 290 290 291 291 292 293 293 294 295 297 298 299 299 290 290 290 290 290 290 290 290		LOU	alu.	λen	Sor	Mot	T.611	Cue	λla	G1 v	Tla	Pro	Aen	Ser	T.ve	T.ve
218 219 220 221 222 23 24		пеп	GIU	ASII	Ser		пец	Cys	ATG	GLY		110	иор	Der	цуз	135
219											100					
220		Asn	Ala	Cvs	Asn	Glv	Asp	Ser	Glv	Glv						
221 222 (2) INFORMATION FOR SEQ ID NO:5: 223 (i) SEQUENCE CHARACTERISTICS: 224 (A) LENGTH: 159 amino acids 225 (B) TYPE: amino acid 226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 251 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 25 264 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 245 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 250 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 256 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty				- 4			-		-	-						
1																
224 (A) LENGTH: 159 amino acids 225 (B) TYPE: amino acid 226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	222	(2)	INFO	ORMA'	NOI	FOR	SEQ	ID 1	NO:5	:						
225 (B) TYPE: amino acid 226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	223	(i)	SEQU	JENCE	CHA	ARAC'	CERI:	STICS	3:							
226 (C) STRANDEDNESS: 227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 250 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 70 75 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	224	(A)	LENC	TH:	159	am:	ino a	acids	3							
227 (D) TOPOLOGY: linear 228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 250 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 70 75 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	225	(B)	TYPE	E: a	amino	aci	id									
228 (ii) MOLECULE TYPE: 229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 250 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 75 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 256 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	226	(C)	STRA	ANDEI	NES	3:										
229 (A) DESCRIPTION: protein 230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 75 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 256 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty	227	` '					ar									
230 (iii) HYPOTHETICAL: no 231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 250 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 75 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 90 256 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty								_								
231 (iv) ANTI-SENSE: no 232 (v) FRAGMENT TYPE: internal 233 (vi) ORIGINAL SOURCE: 234 (vii) IMMEDIATE SOURCE: 235 (viii) POSITION IN GENOME: 236 (ix) FEATURE: 237 (x) PUBLICATION INFORMATION: 238 (xi) SEQUENCE DESCRIPTION:SEQ ID NO: 5: 239 Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Va 240 5 10 15 241 242 Leu Ser Arg Trp Arg Val Phe Ala Gly Ala Val Ala Gln Ala Se 243 20 25 30 244 245 Pro His Gly Leu Gln Leu Gly Val Gln Ala Val Val Tyr His Gl 246 35 40 45 247 248 Gly Tyr Leu Pro Phe Arg Asp Pro Asn Ser Glu Glu Asn Ser As 249 50 55 60 251 Asp Ile Ala Leu Val His Leu Ser Ser Pro Leu Pro Leu Thr Gl 252 65 70 75 253 254 Tyr Ile Gln Pro Val Cys Leu Pro Ala Ala Gly Gln Ala Leu Va 255 80 85 256 257 Asp Gly Lys Ile Cys Thr Val Thr Gly Trp Gly Asn Thr Gln Ty						-		in								
232			-				no									
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Trp Val Leu Thr Ala Ala His Cys Phe Pro Glu Arg Asn Arg Var 240										O NO	: !	5 :				
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